

Applicant: June *et al.*

Serial No.: 09/349,915

Filing Date: July 8, 1999

Title: Methods for Selectively Stimulating
Proliferation of T-Cells

Art Unit: 1636


Examiner: Unassigned

Commissioner for Patents
Washington, DC 20231

CERTIFICATION UNDER 37 C.F.R. § 1.10

I hereby certify that the attached papers are being deposited with the United States Postal Service as "Express Mail Post Office to Addressee" Service under 37 C.F.R. § 1.10 on 17 May 2002 addressed to: **BOX SEQUENCE**, U.S. Patent and Trademark Office, 2011 South Clark Place, Customer Window, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

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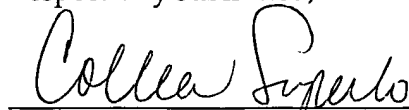

Becky Johnson

STATEMENT UNDER 37 C.F.R. § 1.821(f)

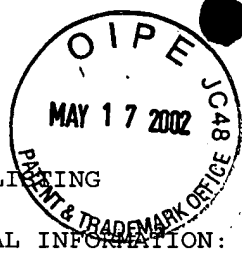
The substitute diskette enclosed herewith contains a computer readable form of the Sequence Listing for the above-referenced patent application. The information recorded in computer readable form on the diskette is identical to the substitute written Sequence Listing. The computer readable form of the Sequence Listing contained on this diskette is understood to comply with the requirements of § 1.821(f).

Respectfully submitted,

Dated: May 17, 2002


Colleen Superko
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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: June, Carl H., Thompson, Craig B., Nabel, Gary J.
Gray, Gary S., Rennert, Paul D.
- (ii) TITLE OF INVENTION: Methods For Selectively Stimulating
Proliferation Of T-Cells
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: HALE AND DORR LLP
 - (B) STREET: 60 State Street
 - (C) CITY: Boston
 - (D) STATE: Massachusetts
 - (E) COUNTRY: USA
 - (F) ZIP: 02109
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/349,915
 - (B) FILING DATE: July 8, 1999
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/403,253
 - (B) FILING DATE: March 10, 1995
 - (A) APPLICATION NUMBER: US 08/253,964
 - (B) FILING DATE: 3 JUNE 1994
 - (A) APPLICATION NUMBER: US 08/073,223
 - (B) FILING DATE: 4 JUNE 1993
 - (A) APPLICATION NUMBER: US 08/200,947
 - (B) FILING DATE: 23 FEB 1994
 - (A) APPLICATION NUMBER: US 07/864,805
 - (B) FILING DATE: 7 APR 1992
 - (A) APPLICATION NUMBER: US 08/247,505
 - (B) FILING DATE: 23 MAY 1994
 - (A) APPLICATION NUMBER: US 07/864,866
 - (B) FILING DATE: 7 APR 1992
 - (A) APPLICATION NUMBER: US 08/218,155
 - (B) FILING DATE: 25 MAR 1994
 - (A) APPLICATION NUMBER: US 07/864,807
 - (B) FILING DATE: 7 APR 1992
 - (A) APPLICATION NUMBER: US 07/902,467
 - (B) FILING DATE: 16 JUNE 1992
 - (A) APPLICATION NUMBER: US 07/275,433
 - (B) FILING DATE: 23 NOV 1988

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Mandragouras, Amy E.
- (B) REGISTRATION NUMBER: 36,207
- (C) REFERENCE/DOCKET NUMBER: RPI-002CP2

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (617) 227-7400
- (B) TELEFAX: (617) 742-4214

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapien
- (F) TISSUE TYPE: lymphoid
- (G) CELL TYPE: B cell
- (H) CELL LINE: Raji

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA in pCDM8 vector
- (B) CLONE: B7, Raji clone #13

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: 3

(ix) FEATURE:

- (A) NAME/KEY: Open reading frame (translated region)
- (B) LOCATION: 318 to 1181 bp
- (C) IDENTIFICATION METHOD: similarity to other pattern

(ix) FEATURE:

- (A) NAME/KEY: Alternate polyadenylation signal
- (B) LOCATION: 1474 to 1479 bp
- (C) IDENTIFICATION METHOD: similarity to other pattern

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: FREEMAN, GORDON J.
FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.

LEE, GRACE
WHITMAN, JAMES F.
NADLER, LEE M.

(B) TITLE: B7, A New Member Of The Ig Superfamily With
Unique Expression On Activated And Neoplastic B Cells
(C) JOURNAL: The Journal of Immunology
(D) VOLUME: 143
(E) ISSUE: 8
(F) PAGES: 2714-2722
(G) DATE: 15-OCT-1989
(H) RELEVANT RESIDUES In SEQ ID NO:1: FROM 1 TO 1491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCAAAGAAAA AGTGATTTGT CATTGCTTTA TAGACTGTAA GAAGAGAACA TCTCAGAAGT	60
GGAGTCTTAC CCTGAAATCA AAGGATTTAA AGAAAAAGTG GAATTTTCTCT TCAGCAAGCT	120
GTGAAACTAA ATCCACAACC TTTGGAGACC CAGGAACACC CTCCAATCTC TGTGTGTTTT	180
GTAAACATCA CTGGAGGGTC TTCTACGTGA GCAATTGGAT TGTCATCAGC CCTGCCTGTT	240
TTGCACCTGG GAAGTGCCCT GGTCTTACTT GGGTCCAAAT TGTTGGCTTT CACTTTTGAC	300
CCTAAGCATC TGAAGCC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA TCC	353
Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser	
-30 -25	
AAG TGT CCA TAC CTG AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT CTT	401
Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu	
-20 -15 -10	
TCT CAC TTC TGT TCA GGT GTT ATC CAC GTG ACC AAG GAA GTG AAA GAA	449
Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu	
-5 1 5 10	
GTG GCA ACG CTG TCC TGT GGT CAC AAT GTT TCT GTT GAA GAG CTG GCA	497
Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala	
15 20 25	
CAA ACT CGC ATC TAC TGG CAA AAG GAG AAG AAA ATG GTG CTG ACT ATG	545
Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met	
30 35 40	
ATG TCT GGG GAC ATG AAT ATA TGG CCC GAG TAC AAG AAC CGG ACC ATC	593
Met Ser Gly Asp Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile	
45 50 55	
TTT GAT ATC ACT AAT AAC CTC TCC ATT GTG ATC CTG GCT CTG CGC CCA	641
Phe Asp Ile Thr Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro	

60	65	70	
TCT GAC GAG GGC ACA TAC GAG TGT GTT GTT CTG AAG TAT GAA AAA GAC Ser Asp Glu Gly Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp 75 80 85 90	689		
GCT TTC AAG CGG GAA CAC CTG GCT GAA GTG ACG TTA TCA GTC AAA GCT Ala Phe Lys Arg Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala 95 100 105	737		
GAC TTC CCT ACA CCT AGT ATA TCT GAC TTT GAA ATT CCA ACT TCT AAT Asp Phe Pro Thr Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn 110 115 120	785		
ATT AGA AGG ATA ATT TGC TCA ACC TCT GGA GGT TTT CCA GAG CCT CAC Ile Arg Arg Ile Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His 125 130 135	833		
CTC TCC TGG TTG GAA AAT GGA GAA GAA TTA AAT GCC ATC AAC ACA ACA Leu Ser Trp Leu Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr 140 145 150	881		
GTT TCC CAA GAT CCT GAA ACT GAG CTC TAT GCT GTT AGC AGC AAA CTG Val Ser Gln Asp Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu 155 160 165 170	929		
GAT TTC AAT ATG ACA ACC AAC CAC AGC TTC ATG TGT CTC ATC AAG TAT Asp Phe Asn Met Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr 175 180 185	977		
GGA CAT TTA AGA GTG AAT CAG ACC TTC AAC TGG AAT ACA ACC AAG CAA Gly His Leu Arg Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln 190 195 200	1025		
GAG CAT TTT CCT GAT AAC CTG CTC CCA TCC TGG GCC ATT ACC TTA ATC Glu His Phe Pro Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile 205 210 215	1073		
TCA GTA AAT GGA ATT TTT GTG ATA TGC TGC CTG ACC TAC TGC TTT GCC Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala 220 225 230	1121		
CCA AGA TGC AGA GAG AGA AGG AGG AAT GAG AGA TTG AGA AGG GAA AGT Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser 235 240 245 250	1169		

GTA CGC CCT GTA TAACAGTGTC CGCAGAAGCA AGGGGCTGAA AAGATCTGAA 1221
 Val Arg Pro Val

GGTAGCCTCC GTCATCTCTT CTGGGATACA TGGATCGTGG GGATCATGAG GCATTCTTCC 1281

CTTAACAAAT TTAAGCTGTT TTACCCACTA CCTCACCTTC TTAAAAACCT CTTTCAGATT 1341

AAGCTGAACA GTTACAAGAT GGCTGGCATC CCTCTCCTTT CTCCCCATAT GCAATTTGCT 1401

TAATGTAACC TCTTCTTTTG CCATGTTTCC ATTCTGCCAT CTTGAATTGT CTTGTCAGCC 1461

AATTCATTAT CTATTAAACA CTAATTTGAG 1491

(3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 288 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: B cell activation antigen; natural ligand
for CD28 T cell surface antigen; transmembrane protein

(ix) FEATURE:

- (A) NAME/KEY: signal sequence
- (B) LOCATION: -34 to -1
- (C) IDENTIFICATION METHOD: amino terminal sequencing of
soluble protein
- (D) OTHER INFORMATION: hydrophobic

(ix) FEATURE:

- (A) NAME/KEY: extracellular domain
- (B) LOCATION: 1 to 208
- (C) IDENTIFICATION METHOD: similarity with known
sequence

(ix) FEATURE:

- (A) NAME/KEY: transmembrane domain
- (B) LOCATION: 209 to 235
- (C) IDENTIFICATION METHOD: similarity with known
sequence

(ix) FEATURE:

- (A) NAME/KEY: intracellular domain
- (B) LOCATION: 236 to 254
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 19 to 21
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 55 to 57
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 64 to 66
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 152 to 154
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 173 to 175
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 177 to 179
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 192 to 194
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 198 to 200
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: Ig V-set domain
- (B) LOCATION: 1 to 104
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: Ig C-set domain
- (B) LOCATION: 105 to 202
- (C) IDENTIFICATION METHOD: similarity with known sequence

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: FREEMAN, GORDON J.
FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
LEE, GRACE
WHITMAN, JAMES F.
NADLER, LEE M.
- (B) TITLE: B7, A New Member Of The Ig Superfamily With Unique Expression On Activated And Neoplastic B Cells
- (C) JOURNAL: The Journal of Immunology
- (D) VOLUME: 143
- (E) ISSUE: 8
- (F) PAGES: 2714-2722
- (G) DATE: 15-OCT-1989
- (H) RELEVANT RESIDUES IN SEQUENCE ID NO:2: From -26 to 262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gly	His	Thr	Arg	Arg	Gln	Gly	Thr	Ser	Pro	Ser	Lys	Cys	Pro	Tyr
				-30					-25					-20	
Leu	Asn	Phe	Phe	Gln	Leu	Leu	Val	Leu	Ala	Gly	Leu	Ser	His	Phe	Cys
				-15				-10						-5	
Ser	Gly	Val	Ile	His	Val	Thr	Lys	Glu	Val	Lys	Glu	Val	Ala	Thr	Leu

-1	1		5		10														
Ser	Cys	Gly	His	Asn	Val	Ser	Val	Glu	Glu	Leu	Ala	Gln	Thr	Arg	Ile				
15					20					25					30				
Tyr	Trp	Gln	Lys	Glu	Lys	Lys	Met	Val	Leu	Thr	Met	Met	Ser	Gly	Asp				
			35						40					45					
Met	Asn	Ile	Trp	Pro	Glu	Tyr	Lys	Asn	Arg	Thr	Ile	Phe	Asp	Ile	Thr				
		50						55					60						
Asn	Asn	Leu	Ser	Ile	Val	Ile	Leu	Ala	Leu	Arg	Pro	Ser	Asp	Glu	Gly				
		65					70						75						
Thr	Tyr	Glu	Cys	Val	Val	Leu	Lys	Tyr	Glu	Lys	Asp	Ala	Phe	Lys	Arg				
	80					85					90								
Glu	His	Leu	Ala	Glu	Val	Thr	Leu	Ser	Val	Lys	Ala	Asp	Phe	Pro	Thr				
95					100					105					110				
Pro	Ser	Ile	Ser	Asp	Phe	Glu	Ile	Pro	Thr	Ser	Asn	Ile	Arg	Arg	Ile				
			115						120					125					
Ile	Cys	Ser	Thr	Ser	Gly	Gly	Phe	Pro	Glu	Pro	His	Leu	Ser	Trp	Leu				
			130					135					140						
Glu	Asn	Gly	Glu	Glu	Leu	Asn	Ala	Ile	Asn	Thr	Thr	Val	Ser	Gln	Asp				
		145					150					155							
Pro	Glu	Thr	Glu	Leu	Tyr	Ala	Val	Ser	Ser	Lys	Leu	Asp	Phe	Asn	Met				
	160					165					170								
Thr	Thr	Asn	His	Ser	Phe	Met	Cys	Leu	Ile	Lys	Tyr	Gly	His	Leu	Arg				
175					180					185					190				
Val	Asn	Gln	Thr	Phe	Asn	Trp	Asn	Thr	Thr	Lys	Gln	Glu	His	Phe	Pro				
				195					200					205					
Asp	Asn	Leu	Leu	Pro	Ser	Trp	Ala	Ile	Thr	Leu	Ile	Ser	Val	Asn	Gly				
		210						215					220						
Ile	Phe	Val	Ile	Cys	Cys	Leu	Thr	Tyr	Cys	Phe	Ala	Pro	Arg	Cys	Arg				
	225						230					235							
Glu	Arg	Arg	Arg	Asn	Glu	Arg	Leu	Arg	Arg	Glu	Ser	Val	Arg	Pro	Val				
	240					245					250								

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1120 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 107..1093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT	60
GAGTGGGGTTC ATTTCCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC	115
Met Asp Pro	
1	
CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG	163
Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu	
5 10 15	
CTC TCT GGT GCT GCT CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT	211
Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr	
20 25 30 35	
GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT	259
Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser	
40 45 50	
GAG CTA GTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG	307
Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu	
55 60 65	
GTA TAC TTA GGC AAA GAG AAA TTT GAC AGT GTT CAT TCC AAG TAT ATG	355
Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met	
70 75 80	
GGC CGC ACA AGT TTT GAT TCG GAC AGT TGG ACC CTG AGA CTT CAC AAT	403
Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn	
85 90 95	
CTT CAG ATC AAG GAC AAG GGC TTG TAT CAA TGT ATC ATC CAT CAC AAA	451
Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys	
100 105 110 115	
AAG CCC ACA GGA ATG ATT CGC ATC CAC CAG ATG AAT TCT GAA CTG TCA	499
Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser	
120 125 130	
GTG CTT GCT AAC TTC AGT CAA CCT GAA ATA GTA CCA ATT TCT AAT ATA	547
Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile	
135 140 145	
ACA GAA AAT GTG TAC ATA AAT TTG ACC TGC TCA TCT ATA CAC GGT TAC	595
Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr	
150 155 160	
CCA GAA CCT AAG AAG ATG AGT GTT TTG CTA AGA ACC AAG AAT TCA ACT	643

Pro	Glu	Pro	Lys	Lys	Met	Ser	Val	Leu	Leu	Arg	Thr	Lys	Asn	Ser	Thr	
165						170					175					
ATC	GAG	TAT	GAT	GGT	ATT	ATG	CAG	AAA	TCT	CAA	GAT	AAT	GTC	ACA	GAA	691
Ile	Glu	Tyr	Asp	Gly	Ile	Met	Gln	Lys	Ser	Gln	Asp	Asn	Val	Thr	Glu	
180					185					190					195	
CTG	TAC	GAC	GTT	TCC	ATC	AGC	TTG	TCT	GTT	TCA	TTC	CCT	GAT	GTT	ACG	739
Leu	Tyr	Asp	Val	Ser	Ile	Ser	Leu	Ser	Val	Ser	Phe	Pro	Asp	Val	Thr	
				200					205					210		
AGC	AAT	ATG	ACC	ATC	TTC	TGT	ATT	CTG	GAA	ACT	GAC	AAG	ACG	CGG	CTT	787
Ser	Asn	Met	Thr	Ile	Phe	Cys	Ile	Leu	Glu	Thr	Asp	Lys	Thr	Arg	Leu	
			215					220					225			
TTA	TCT	TCA	CCT	TTC	TCT	ATA	GAG	CTT	GAG	GAC	CCT	CAG	CCT	CCC	CCA	835
Leu	Ser	Ser	Pro	Phe	Ser	Ile	Glu	Leu	Glu	Asp	Pro	Gln	Pro	Pro	Pro	
			230				235					240				
GAC	CAC	ATT	CCT	TGG	ATT	ACA	GCT	GTA	CTT	CCA	ACA	GTT	ATT	ATA	TGT	883
Asp	His	Ile	Pro	Trp	Ile	Thr	Ala	Val	Leu	Pro	Thr	Val	Ile	Ile	Cys	
	245					250					255					
GTG	ATG	GTT	TTC	TGT	CTA	ATT	CTA	TGG	AAA	TGG	AAG	AAG	AAG	AAG	CGG	931
Val	Met	Val	Phe	Cys	Leu	Ile	Leu	Trp	Lys	Trp	Lys	Lys	Lys	Lys	Arg	
260					265				270						275	
CCT	CGC	AAC	TCT	TAT	AAA	TGT	GGA	ACC	AAC	ACA	ATG	GAG	AGG	GAA	GAG	979
Pro	Arg	Asn	Ser	Tyr	Lys	Cys	Gly	Thr	Asn	Thr	Met	Glu	Arg	Glu	Glu	
				280					285					290		
AGT	GAA	CAG	ACC	AAG	AAA	AGA	GAA	AAA	ATC	CAT	ATA	CCT	GAA	AGA	TCT	1027
Ser	Glu	Gln	Thr	Lys	Lys	Arg	Glu	Lys	Ile	His	Ile	Pro	Glu	Arg	Ser	
			295					300					305			
GAT	GAA	GCC	CAG	CGT	GTT	TTT	AAA	AGT	TCG	AAG	ACA	TCT	TCA	TGC	GAC	1075
Asp	Glu	Ala	Gln	Arg	Val	Phe	Lys	Ser	Ser	Lys	Thr	Ser	Ser	Cys	Asp	
	310						315					320				
AAA	AGT	GAT	ACA	TGT	TTT	TAATTAAAGA	GTAAAGCCCA	AAAAAAA								1120
Lys	Ser	Asp	Thr	Cys	Phe											
	325															

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asp	Pro	Gln	Cys	Thr	Met	Gly	Leu	Ser	Asn	Ile	Leu	Phe	Val	Met	
1				5				10					15			

Ala	Phe	Leu	Leu	Ser	Gly	Ala	Ala	Pro	Leu	Lys	Ile	Gln	Ala	Tyr	Phe		
		20						25					30				
Asn	Glu	Thr	Ala	Asp	Leu	Pro	Cys	Gln	Phe	Ala	Asn	Ser	Gln	Asn	Gln		
		35					40					45					
Ser	Leu	Ser	Glu	Leu	Val	Val	Phe	Trp	Gln	Asp	Gln	Glu	Asn	Leu	Val		
	50					55					60						
Leu	Asn	Glu	Val	Tyr	Leu	Gly	Lys	Glu	Lys	Phe	Asp	Ser	Val	His	Ser		
	65				70					75					80		
Lys	Tyr	Met	Gly	Arg	Thr	Ser	Phe	Asp	Ser	Asp	Ser	Trp	Thr	Leu	Arg		
				85					90					95			
Leu	His	Asn	Leu	Gln	Ile	Lys	Asp	Lys	Gly	Leu	Tyr	Gln	Cys	Ile	Ile		
		100						105					110				
His	His	Lys	Lys	Pro	Thr	Gly	Met	Ile	Arg	Ile	His	Gln	Met	Asn	Ser		
		115					120					125					
Glu	Leu	Ser	Val	Leu	Ala	Asn	Phe	Ser	Gln	Pro	Glu	Ile	Val	Pro	Ile		
	130					135					140						
Ser	Asn	Ile	Thr	Glu	Asn	Val	Tyr	Ile	Asn	Leu	Thr	Cys	Ser	Ser	Ile		
	145				150					155					160		
His	Gly	Tyr	Pro	Glu	Pro	Lys	Lys	Met	Ser	Val	Leu	Leu	Arg	Thr	Lys		
				165					170					175			
Asn	Ser	Thr	Ile	Glu	Tyr	Asp	Gly	Ile	Met	Gln	Lys	Ser	Gln	Asp	Asn		
		180						185					190				
Val	Thr	Glu	Leu	Tyr	Asp	Val	Ser	Ile	Ser	Leu	Ser	Val	Ser	Phe	Pro		
	195						200					205					
Asp	Val	Thr	Ser	Asn	Met	Thr	Ile	Phe	Cys	Ile	Leu	Glu	Thr	Asp	Lys		
	210					215					220						
Thr	Arg	Leu	Leu	Ser	Ser	Pro	Phe	Ser	Ile	Glu	Leu	Glu	Asp	Pro	Gln		
	225				230					235					240		
Pro	Pro	Pro	Asp	His	Ile	Pro	Trp	Ile	Thr	Ala	Val	Leu	Pro	Thr	Val		
				245					250					255			
Ile	Ile	Cys	Val	Met	Val	Phe	Cys	Leu	Ile	Leu	Trp	Lys	Trp	Lys	Lys		
		260						265					270				
Lys	Lys	Arg	Pro	Arg	Asn	Ser	Tyr	Lys	Cys	Gly	Thr	Asn	Thr	Met	Glu		
		275					280					285					
Arg	Glu	Glu	Ser	Glu	Gln	Thr	Lys	Lys	Arg	Glu	Lys	Ile	His	Ile	Pro		
	290					295					300						
Glu	Arg	Ser	Asp	Glu	Ala	Gln	Arg	Val	Phe	Lys	Ser	Ser	Lys	Thr	Ser		

305

310

315

320

Ser Cys Asp Lys Ser Asp Thr Cys Phe
325

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label=Xaa is any amino acid

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /label=Xaa is any amino acid

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /label=Xaa is any amino acid

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /label=Xaa is any amino acid

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /label=Xaa is Asp or Glu

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /label=Xaa is any amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Xaa Gly Xaa Trp Leu Xaa Xaa Xaa Xaa
5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Pro Val Lys Gly Gly Thr Lys Cys Ile Lys Tyr Leu Leu Phe Gly Phe
 5 10 15

Asn Phe Ile Phe Trp Leu Ala Gly Ile Ala Val Leu Ala Ile Gly Leu
 20 25 30

Trp Leu Arg Phe Asp Ser Gln Thr Lys Ser Ile Phe Glu Gln Glu Thr
 35 40 45

Asn Asn Asn Asn Ser Ser Phe Tyr Thr Gly Val Tyr Ile Leu Ile Gly
 50 55 60

Ala Gly Ala Leu Met Met Leu Val Gly Phe Leu Gly Cys Cys Gly Ala
 65 70 75 80

Val Gln Glu Ser Gln Cys Met Leu Gly Leu Phe Phe Gly Phe Leu Leu
 85 90 95

Val Ile Phe Ala Ile Glu Ile Ala Ala Ala Ile Trp Gly Tyr Ser His
 100 105 110

Lys Asp Glu Val Ile Lys Glu Val Gln Glu Phe Tyr Lys Asp Thr Tyr
 115 120 125

Asn Lys Leu Lys Thr Lys Asp Glu Pro Gln Arg Glu Thr Leu Lys Ala
 130 135 140

Ile His Tyr Ala Leu Asn Cys Cys Gly Leu Ala Gly Gly Val Glu Gln
 145 150 155 160

Phe Ile Ser Asp Ile Cys Pro Lys Lys Asp Val Leu Glu Thr Phe Thr
 165 170 175

Val Lys Ser Cys Pro Asp Ala Ile Lys Glu Val Phe Asp Asn Lys Phe
 180 185 190

His Ile Ile Gly Ala Val Gly Ile Gly Ile Ala Val Val Met Ile Phe
 195 200 205

Gly Met Ile Phe Ser Met Ile Leu Cys Cys Ala Ile Arg Arg Asn Arg
 210 215 220

Glu Met Val
225

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Leu Trp Leu Arg Phe Asp
1 5

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

His Gln Phe Cys Asp His Trp Gly Cys Trp Leu Leu Arg Glu Thr His
1 5 10 15

Ile Phe Thr Pro
20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu Arg Leu Val Leu Glu Asp Pro Gly Ile Trp Leu Arg Pro Asp Tyr
1 5 10 15

Phe Phe Pro Ala
20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Cys Trp Leu Arg Glu
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gly Ile Trp Leu Arg Pro Asp
1 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 2
(D) OTHER INFORMATION: /label=Xaa is any amino acid

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 5
(D) OTHER INFORMATION: /label=Xaa is any amino acid

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 6
(D) OTHER INFORMATION: /label=Xaa is Asp or Glu

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly Xaa Trp Leu Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTTTAGAGCA CA

12

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCTAAAG

8